

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Kaushansky, Kenneth

(ii) TITLE OF INVENTION: Methods of Stimulating Erythropoiesis  
Using Hematopoietic Proteins.

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: ZymoGenetics, Inc.
- (B) STREET: 1201 Eastlake Avenue East
- (C) CITY: Seattle
- (D) STATE: WA
- (E) COUNTRY: USA
- (F) ZIP: 98102

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Parker, Gary E
- (B) REGISTRATION NUMBER: 31-648
- (C) REFERENCE/DOCKET NUMBER: 94-09C2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 206-442-6673
- (B) TELEFAX: 206-442-6678

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..1059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GAG CTG ACT GAA TTG CTC CTC GTG GTC ATG CTT CTC CTA ACT GCA Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala 1 5 10 15	48
AGG CTA ACG CTG TCC AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val 20 25 30	96
CTC AGT AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG AGC Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser 35 40 45	144
CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC CTG CTG CCT GCT Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala 50 55 60	192
GTG GAC TTT AGC TTG GGA GAA TGG AAA ACC CAG ATG GAG GAG ACC AAG Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys 65 70 75 80	240
GCA CAG GAC ATT CTG GGA GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met 85 90 95	288
GCA GCA CGG GGA CAA CTG GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly 100 105 110	336
CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG GCC CTG CAG AGC CTC Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu 115 120 125	384

CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG ACC ACA GCT CAC AAG GAT			432
Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp			
130	135	140	
CCC AAT GCC ATC TTC CTG AGC TTC CAA CAC CTG CTC CGA GGA AAG GTG			480
Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val			
145	150	155	160
CGT TTC CTG ATG CTT GTA GGA GGG TCC ACC CTC TGC GTC AGG CGG GCC			528
Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala			
165	170	175	
CCA CCC ACC ACA GCT GTC CCC AGC AGA ACC TCT CTA GTC CTC ACA CTG			576
Pro Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu			
180	185	190	
AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG TTG GAG ACA AAC TTC ACT			624
Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr			
195	200	205	
GCC TCA GCC AGA ACT ACT GGC TCT GGG CTT CTG AAG TGG CAG CAG GGA			672
Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly			
210	215	220	
TTC AGA GCC AAG ATT CCT GGT CTG CTG AAC CAA ACC TCC AGG TCC CTG			720
Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu			
225	230	235	240
GAC CAA ATC CCC GGA TAC CTG AAC AGG ATA CAC GAA CTC TTG AAT GGA			768
Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly			
245	250	255	
ACT CGT GGA CTC TTT CCT GGA CCC TCA CGC AGG ACC CTA GGA GCC CCG			816
Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro			
260	265	270	
GAC ATT TCC TCA GGA ACA TCA GAC ACA GGC TCC CTG CCA CCC AAC CTC			864
Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu			
275	280	285	
CAG CCT GGA TAT TCT CCT TCC CCA ACC CAT CCT ACT GGA CAG TAT			912
Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr			
290	295	300	

ACG CTC TTC CCT CTT CCA CCC ACC TTG CCC ACC CCT GTG GTC CAG CTC	960																						
Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu																							
305	310	315	320	CAC CCC CTG CTT CCT GAC CCT TCT GCT CCA ACG CCC ACC CCT ACC AGC	1008	His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser		325	330	335		CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC CAG AAT CTG TCT CAG GAA	1056	Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu		340	345	350		GGG TAA	1062	Gly	
315	320																						
CAC CCC CTG CTT CCT GAC CCT TCT GCT CCA ACG CCC ACC CCT ACC AGC	1008																						
His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser																							
325	330	335		CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC CAG AAT CTG TCT CAG GAA	1056	Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu		340	345	350		GGG TAA	1062	Gly									
335																							
CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC CAG AAT CTG TCT CAG GAA	1056																						
Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu																							
340	345	350		GGG TAA	1062	Gly																	
350																							
GGG TAA	1062																						
Gly																							

**(2) INFORMATION FOR SEQ ID NO:2:**

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

**(ii) MOLECULE TYPE: protein**

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:**

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala																																	
1	5	10	15	Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val		20	25	30		Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser		35	40	45		Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala		50	55	60		Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys		65	70	75	80	Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met		85	90	95	
10	15																																
Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val																																	
20	25	30		Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser		35	40	45		Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala		50	55	60		Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys		65	70	75	80	Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met		85	90	95							
30																																	
Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser																																	
35	40	45		Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala		50	55	60		Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys		65	70	75	80	Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met		85	90	95													
45																																	
Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala																																	
50	55	60		Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys		65	70	75	80	Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met		85	90	95																			
60																																	
Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys																																	
65	70	75	80	Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met		85	90	95																									
75	80																																
Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met																																	
85	90	95																															
95																																	

Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly  
 100 105 110

Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu  
 115 120 125

Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp  
 130 135 140

Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val  
 145 150 155 160

Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala  
 165 170 175

Pro Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu  
 180 185 190

Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr  
 195 200 205

Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly  
 210 215 220

Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu  
 225 230 235 240

Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly  
 245 250 255

Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro  
 260 265 270

Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu  
 275 280 285

Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr  
 290 295 300

Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu  
 305 310 315 320

His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser  
 325 330 335

Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu  
 340 345 350

Gly

(2) INFORMATION FOR SEQ ID NO:3:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

**(vi) IMMEDIATE SOURCE:**

(B) CLONE: 1081

**(ix) FEATURE:**

(A) NAME/KEY: CDS  
(B) LOCATION: 105..1241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTCGTGCCG GTCCTGAGGC CCTTCTCCAC CCGGACAGAG TCCTTGGCCC ACCTCTCTCC 60

CACCCGACTC TGCCGAAAGA AGCACAGAAG CTCAAGCCGC CTCC ATG GCC CCA GGA 116

Met Ala Pro Gly

1

AAG ATT CAG GGG AGA GGC CCC ATA CAG GGA GCC ACT TCA GTT AGA CAC 164  
 Lys Ile Gln Gly Arg Gly Pro Ile Gln Gly Ala Thr Ser Val Arg His

CTG GCC AGA ATG GAG CTG ACT GAT TTG CTC CTG GCG GCC ATG CTT CTT 212  
 Leu Ala Arg Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu  
 35 39 35

GCA GTG GCA AGA CTA ACT CTG TCC AGC CCC GTA GCT CCT GCC TGT GAC 260  
 Ala Val Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp  
 40 45 50

CCC AGA CTC CTA AAT AAA CTG CTG CGT GAC TCC CAC CTC CTT CAC AGC			308
Pro Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser			
55	60	65	
CGA CTG AGT CAG TGT CCC GAC GTC GAC CCT TTG TCT ATC CCT GTT CTG			356
Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val Leu			
70	75	80	
CTG CCT GCT GTG GAC TTT AGC CTG GGA GAA TGG AAA ACC CAG ACG GAA			404
Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu			
85	90	95	100
CAG AGC AAG GCA CAG GAC ATT CTA GGG GCA GTG TCC CTT CTA CTG GAG			452
Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Leu Glu			
105	110	115	
GGA GTG ATG GCA GCA CGA GGA CAG TTG GAA CCC TCC TGC CTC TCA TCC			500
Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys Leu Ser Ser			
120	125	130	
CTC CTG GGA CAG CTT TCT GGG CAG GTT CGC CTC CTC TTG GGG GCC CTG			548
Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu			
135	140	145	
CAG GGC CTC CTA GGA ACC CAG CTT CCT CTA CAG GGC AGG ACC ACA GCT			596
Gln Gly Leu Leu Gly Thr Gln Leu Pro Leu Gln Gly Arg Thr Thr Ala			
150	155	160	
CAC AAG GAC CCC AAT GCC CTC TTC TTG AGC TTG CAA CAA CTG CTT CGG			644
His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln Gln Leu Leu Arg			
165	170	175	180
GGA AAG GTG CGC TTC CTG CTT CTG GTA GAA GGT CCC ACC CTC TGT GTC			692
Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro Thr Leu Cys Val			
185	190	195	
AGA CGG ACC CTG CCA ACC ACA GCT GTC CCA AGC AGT ACT TCT CAA CTC			740
Arg Arg Thr Leu Pro Thr Thr Ala Val Pro Ser Ser Thr Ser Gln Leu			
200	205	210	
CTC ACA CTA AAC AAG TTC CCA AAC AGG ACT TCT GGA TTG TTG GAG ACG			788
Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr			
215	220	225	

AAC TTC AGT GTC ACA GCC AGA ACT GCT GGC CCT GGA CTT CTG AGC AGG			836
Asn Phe Ser Val Thr Ala Arg Thr Ala Gly Pro Gly Leu Leu Ser Arg			
230	235	240	
CTT CAG GGA TTC AGA GTC AAG ATT ACT CCT GGT CAG CTA AAT CAA ACC			884
Leu Gln Gly Phe Arg Val Lys Ile Thr Pro Gly Gln Leu Asn Gln Thr			
245	250	255	260
TCC AGG TCC CCA GTC CAA ATC TCT GGA TAC CTG AAC AGG ACA CAC GGA			932
Ser Arg Ser Pro Val Gln Ile Ser Gly Tyr Leu Asn Arg Thr His Gly			
265	270	275	
CCT GTG AAT GGA ACT CAT GGG CTC TTT GCT GGA ACC TCA CTT CAG ACC			980
Pro Val Asn Gly Thr His Gly Leu Phe Ala Gly Thr Ser Leu Gln Thr			
280	285	290	
CTG GAA GCC TCA GAC ATC TCG CCC GGA GCT TTC AAC AAA GGC TCC CTG			1028
Leu Glu Ala Ser Asp Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu			
295	300	305	
GCA TTC AAC CTC CAG GGT GGA CTT CCT TCT CCA AGC CTT GCT CCT			1076
Ala Phe Asn Leu Gln Gly Gly Leu Pro Pro Ser Pro Ser Leu Ala Pro			
310	315	320	
GAT GGA CAC ACA CCC TTC CCT CCT TCA CCT GCC TTG CCC ACC ACC CAT			1124
Asp Gly His Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His			
325	330	335	340
GGA TCT CCA CCC CAG CTC CAC CCC CTG TTT CCT GAC CCT TCC ACC ACC			1172
Gly Ser Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro Ser Thr Thr			
345	350	355	
ATG CCT AAC TCT ACC GCC CCT CAT CCA GTC ACA ATG TAC CCT CAT CCC			1220
Met Pro Asn Ser Thr Ala Pro His Pro Val Thr Met Tyr Pro His Pro			
360	365	370	
AGG AAT TTG TCT CAG GAA ACA TAGCGCGGC ACTGGCCCAG TGAGCGTCTG			1271
Arg Asn Leu Ser Gln Glu Thr			
375			
CAGCTTCTCT CGGGGACAAG CTTCCCCAGG AAGGCTGAGA GGCAGCTGCA TCTGCTCCAG			1331
ATGTTCTGCT TTCACCTAAA AGGCCCTGGG GAAGGGATAC ACAGCACTGG AGATTGTAAA			1391

ATTTTAGGAG CTATTTTTT TTAACCTATC AGCAATATTC ATCAGAGCAG CTAGCGATCT	1451
TTGGTCTATT TTGGTATAA ATTTGAAAAT CACTA	1486

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Pro Gly Lys Ile Gln Gly Arg Gly Pro Ile Gln Gly Ala Thr			
1	5	10	15
Ser Val Arg His Leu Ala Arg Met Glu Leu Thr Asp Leu Leu Leu Ala			
20	25	30	
Ala Met Leu Leu Ala Val Ala Arg Leu Thr Leu Ser Ser Pro Val Ala			
35	40	45	
Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu Arg Asp Ser His			
50	55	60	
Leu Leu His Ser Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser			
65	70	75	80
Ile Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys			
85	90	95	
Thr Gln Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser			
100	105	110	
Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser			
115	120	125	
Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu			
130	135	140	

Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Leu Pro Leu Gln Gly  
 145 150 155 160

Arg Thr Thr Ala His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln  
 165 170 175

Gln Leu Leu Arg Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro  
 180 185 190

Thr Leu Cys Val Arg Arg Thr Leu Pro Thr Thr Ala Val Pro Ser Ser  
 195 200 205

Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr Ser Gly  
 210 215 220

Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala Gly Pro Gly  
 225 230 235 240

Leu Leu Ser Arg Leu Gln Gly Phe Arg Val Lys Ile Thr Pro Gly Gln  
 245 250 255

Leu Asn Gln Thr Ser Arg Ser Pro Val Gln Ile Ser Gly Tyr Leu Asn  
 260 265 270

Arg Thr His Gly Pro Val Asn Gly Thr His Gly Leu Phe Ala Gly Thr  
 275 280 285

Ser Leu Gln Thr Leu Glu Ala Ser Asp Ile Ser Pro Gly Ala Phe Asn  
 290 295 300

Lys Gly Ser Leu Ala Phe Asn Leu Gln Gly Gly Leu Pro Pro Ser Pro  
 305 310 315 320

Ser Leu Ala Pro Asp Gly His Thr Pro Phe Pro Pro Ser Pro Ala Leu  
 325 330 335

Pro Thr Thr His Gly Ser Pro Pro Gln Leu His Pro Leu Phe Pro Asp  
 340 345 350

Pro Ser Thr Thr Met Pro Asn Ser Thr Ala Pro His Pro Val Thr Met  
 355 360 365

Tyr Pro His Pro Arg Asn Leu Ser Gln Glu Thr  
 370 375

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(632..644, 876..1003, 1290..1376, 3309..3476, 3713..4375)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTTCTTGCT TTCTTCTTCTT CTTCTTTCT TTCTTTTTTT TTTTGAGAC GGAGTTCAC	60
TCTTATTGCC CAGGCTGGAG TGCAATGGTG CGATCTCGGC TCACCACAAAC CTCCGCCTCC	120
CAGGTACAAG CGATTCTCCT GTCTCAGCCT CCCAAGTAGC TTGGATTACA GGCATGAACC	180
ACCACACCCCT GCTAGTTTTT TTGTATTCG TAGAGCCGGG GTTTCACCAT GTTAGTGAGG	240
CTGGTGGCGA ACTCCTGACC TCAGGTGATC CACCCGCCTT GGACTCCAA AGTGCTGGGA	300
TTACAGGCAT GAGCCACTGC ACCCGGCACA CCATATGCTT TCATCACAAG AAAATGTGAG	360
AGAATTCAAG GCTTTGGCAG TTCCAGGCTG GTCAGCATCT CAAGCCCTCC CCAGCATCTG	420
TTCACCCCTGC CAGGCAGTCT CTTCTAGAA ACTTGGTTAA ATGTTCACTC TTCTTGCTAC	480
TTTCAGGATA GATTCTTCAC CCTTGGTCCG CCTTTGCCCC ACCCTACTCT GCCCAGAAGT	540
GCAAGAGCCT AAGCCGCCTC CATGGCCCCA GGAAGGATTC AGGGGAGAGG CCCCAAACAG	600
GGAGCCACGC CAGCCAGACA CCCCGGCCAG A ATG GAG CTG ACT G GTGAGAACAC	654
Met Glu Leu Thr	
1	
ACCTGAGGGG CTAGGGCCAT ATGGAAACAT GACAGAAGGG GAGAGAGAAA GGAGACACGC	714

TGCAGGGGGC AGGAAGCTGG GGGAACCAT TCTCCAAAAA ATAAGGGGTC TGAGGGGTGG	774
ATTCCCTGGG TTTCAGGTCT GGGTCTGAA TGGGAATTCC TGGAATACCA GCTGACAATG	834
ATTCCTCCT CATCTTCAA CCTCACCTCT CCTCATCTAA G AA TTG CTC CTC Glu Leu Leu Leu 5	886
GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC CCG GCT Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser Pro Ala 10 15 20	934
CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT GAC TCC Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser 25 30 35 40	982
CAT GTC CTT CAC AGC AGA CTG GTGAGAACTC CCAACATTAT CCCCTTTATC His Val Leu His Ser Arg Leu 45	1033
CGCGTAACTG GTAAGACACC CATACTCCCA GGAAGACACC ATCACTTCCT CTAACTCCTT	1093
GACCCAATGA CTATTCTTCC CATATTGTCC CCACCTACTG ATCACACTCT CTGACAAGGA	1153
TTATTCTTCA CAATACAGCC CGCATTAAA AGCTCTCGTC TAGAGATAGT ACTCATGGAG	1213
GACTAGCCTG CTTATTAGGC TACCATAGCT CTCTCTATT CAGCTCCCTT CTCCCCCAC	1273
CAATTTTT CAACAG AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr 50 55	1322
CCT GTC CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA ACC Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr 60 65 70	1370
CAG ATG GTAAGAAAGC CATCCCTAAC CTTGGCTTCC CTAAGTCCTG TCTTCAGTTT Gln Met 75	1426
CCCACTGCTT CCCATGGATT CTCCAACATT CTTGAGCTTT TTAAAAATAT CTCACCTTCA	1486
GCTTGGCCAC CCTAACCCAA TCTACATTCA CCTATGATGA TAGCCTGTGG ATAAGATGAT	1546
GGCTTGCAGG TCCAATATGT GAATAGATT GAAGCTGAAC ACCATGAAAAA GCTGGAGAGA	1606

AATCGCTCAT GGCCATGCCT TTGACCTATT CCCGTTCACT CTTCTTAAAT TGGCATGAAG	1666
AAGCAAGACT CATATGTCAT CCACAGATGA CACAAAGCTG GGAAGTACCA CTAAAATAAC	1726
AAAAGACTGA ATCAAGATTG AAATCACTGA AAGACTAGGT CAAAAACAAG GTGAAACAAC	1786
AGAGATATAA ACTTCTACAT GTGGGCCGGG GGCTCACGCC TGTAATCCCA GCACTTTGGG	1846
AGGCCGAGGC AGGCAGATCA CCTGAGGGCA GGAGTTGAG AGCAGCCTGG CCAACATGGC	1906
GAAACCCCGT CTCTACTAAG AATACAGAAT TAGCCGGGCA TGGTAGTGCA TGCTGTAAT	1966
CCCAGCTACT TGGAAGGCTG AAGCAGGAGA ATCCCTTGAA CCCAGGAGGT GGAGGTTGTA	2026
GTGAGCTGAG ATCATGCCAA TGCACCCAG CCTGGGTGAC AAGAGCAAAA CTCCGTCTCA	2086
AAAAGAAAAA AAAATTCTAC ATGTGTAAT TAATGAGTAA AGTCCTATTG CAGCTTCAG	2146
GCCACAATGC CCTGCTTCCA TCATTTAACG CTCTGGCCCT AGCACTTCCT ACGAAAAGGA	2206
TCTGAGAGAA TTAAATTGCC CCCAAACTTA CCATGTAACA TTACTGAAGC TGCTATTCTT	2266
AAAGCTAGTA ATTCTTGCT GTTGATGTT TAGCATCCCC ATTGTGGAAA TGCTCGTACA	2326
GAACCTTATT CCGAGTGGAC TACACTAAA TATACTGGCC TGAACACCGG ACATCCCCCT	2386
GAAGACATAT GCTAATTAT TAAGAGGGAC CATATTAAAC TAACATGTGT CTAGAAAGCA	2446
GCAGCCTGAA CAGAAAGAGA CTAGAACAT GTTTTATGGG CAATAGTTA AAAAACTAAA	2506
ATCTATCCTC AAGAACCTA GCGTCCCTTC TTCCCTCAGG ACTGAGTCAG GGAAGAAGGG	2566
CAGTTCCAT GGGTCCCTTC TAGTCCTTTC TTTTCATCCT TATGATCATT ATGGTAGAGT	2626
CTCATAACCTA CATTAGTTT ATTTATTATT ATTATTTGAG ACGGAGTCTC ACTCTATCCC	2686
CCAGGCTGGA GTGCAGTGGC ATGATCTAA CTCACTGCAA CCTCAGCCTC CCGGATTCAA	2746
GCGATTCTCC TGTCTCAGTC TCCCAAGTAG CTGGGATTAC AGGTGCCAC CACCATGCC	2806
AGCTAATTG TGTATTGTG GTAGAGATGG GGTTTCACCA TGTTGGCAG GCTGATCTG	2866
AACTCCTGAC CTCAGGTGAT CCACCTGCCT CAGCCTCCCA AAGTGCTGGG ATTACAGGCG	2926



CTT	GTA	GGA	GGG	TCC	ACC	CTC	TGC	GTC	AGG	CGG	GCC	CCA	CCC	ACC	ACA	3856
Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg	Ala	Pro	Pro	Thr	Thr	
165				170					175					180		
GCT	GTC	CCC	AGC	AGA	ACC	TCT	CTA	GTC	CTC	ACA	CTG	AAC	GAG	CTC	CCA	3904
Ala	Val	Pro	Ser	Arg	Thr	Ser	Leu	Val	Leu	Thr	Leu	Asn	Glu	Leu	Pro	
185				190					195							
AAC	AGG	ACT	TCT	GGA	TTG	TTG	GAG	ACA	AAC	TTC	ACT	GCC	TCA	GCC	AGA	3952
Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr	Asn	Phe	Thr	Ala	Ser	Ala	Arg	
200				205					210							
ACT	ACT	GGC	TCT	GGG	CTT	CTG	AAG	TGG	CAG	CAG	GGA	TTC	AGA	GCC	AAG	4000
Thr	Thr	Gly	Ser	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	Arg	Ala	Lys	
215				220					225							
ATT	CCT	GGT	CTG	CTG	AAC	CAA	ACC	TCC	AGG	TCC	CTG	GAC	CAA	ATC	CCC	4048
Ile	Pro	Gly	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	Asp	Gln	Ile	Pro	
230				235					240							
GGA	TAC	CTG	AAC	AGG	ATA	CAC	GAA	CTC	TTG	AAT	GGA	ACT	CGT	GGA	CTC	4096
Gly	Tyr	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	Gly	Thr	Arg	Gly	Leu	
245				250					255				260			
TTT	CCT	GGA	CCC	TCA	CGC	AGG	ACC	CTA	GGA	GCC	CCG	GAC	ATT	TCC	TCA	4144
Phe	Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly	Ala	Pro	Asp	Ile	Ser	Ser	
265				270					275							
GGA	ACA	TCA	GAC	ACA	GGC	TCC	CTG	CCA	CCC	AAC	CTC	CAG	CCT	GGA	TAT	4192
Gly	Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro	Pro	Asn	Leu	Gln	Pro	Gly	Tyr	
280				285					290							
TCT	CCT	TCC	CCA	ACC	CAT	CCT	ACT	GGA	CAG	TAT	ACG	CTC	TTC	CCT		4240
Ser	Pro	Ser	Pro	Thr	His	Pro	Pro	Thr	Gly	Gln	Tyr	Thr	Leu	Phe	Pro	
295				300					305							
CTT	CCA	CCC	ACC	TTG	CCC	ACC	CCT	GTG	GTC	CAG	CTC	CAC	CCC	CTG	CTT	4288
Leu	Pro	Pro	Thr	Leu	Pro	Thr	Pro	Val	Val	Gln	Leu	His	Pro	Leu	Leu	
310				315					320							
CCT	GAC	CCT	TCT	GCT	CCA	ACG	CCC	ACC	CCT	ACC	AGC	CCT	CTT	CTA	AAC	4336
Pro	Asp	Pro	Ser	Ala	Pro	Thr	Pro	Thr	Pro	Thr	Ser	Pro	Leu	Leu	Asn	
325				330					335				340			

ACA TCC TAC ACC CAC TCC CAG AAT CTG TCT CAG GAA GGG TAAGGTTCTC	4385
Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu Gly	
345	350
AGACACTGCC GACATCAGCA TTGTCTCGTG TACAGCTCCC TTCCCTGCAG GGCGCCCCCTG	4445
GGAGACAACG GGACAAGATT TCCTACTTTC TCCTGAAACC CAAAGCCCTG GTAAAAGGGA	4505
TACACAGGAC TGAAAAGGGA ATCATTTC ACTGTACATT ATAAACCTTC AGAAGCTATT	4565
TTTTAAGCT ATCAGCAATA CTCATCAGAG CAGCTAGCTC TTTGGTCTAT TTTCTGCAGA	4625
AATTGCAAC TCACTGATT C TCAACATGCT CTTTTCTGT GATAACTCTG CAAAGACCTG	4685
GGCTGGCCTG GCAGTTAAC AGAGGGAGAG ACTAACCTTG AGTCAGAAAA CAGAGGAAGG	4745
GTAATTCCT TTGCTTCAAA TTCAAGGCCT TCCAACGCC CCATCCCTT TACTATCATT	4805
CTCAGTGGGA CTCTGATC	4823

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala			
1	5	10	15
Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val			
20	25	30	
Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser			
35	40	45	
Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala			
50	55	60	

Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys  
 65 70 75 80

Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met  
 85 90 95

Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly  
 100 105 110

Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu  
 115 120 125

Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp  
 130 135 140

Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val  
 145 150 155 160

Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala  
 165 170 175

Pro Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu  
 180 185 190

Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr  
 195 200 205

Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly  
 210 215 220

Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu  
 225 230 235 240

Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly  
 245 250 255

Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro  
 260 265 270

Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu  
 275 280 285

Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr  
 290 295 300

Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu  
305 310 315 320

His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser  
325 330 335

Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu  
340 345 350

Gly